Docket No. CEN0250NP

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent of	:	George Heavner, *et al.*	Patent No.: 7,250,165
Serial No.	:	09/920,137	Art Unit: 1647
Filed	:	August 1, 2001	Examiner: Seharaseyon, Jegatheesan
Title	:	Anti-TNF Antibodies, Compositions, Methods And Uses	

Attention: Certificate of Corrections Branch
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

REQUEST FOR CERTIFICATE OF CORRECTION UNDER 37 C.F.R .§1.322

Dear Sir:

Transmitted herewith is a Certificate of Correction for U.S. Patent 7,250,265, issued July 31, 2007. Upon review of the patent, the patentees noticed that the sequence listing published with the above-referenced patent does not correspond to the sequence listing provided to the U.S. Patent and Trademark Office, as set forth in the image file wrapper provided on PAIR (see January 17, 2006 sequence listing). The patentees submit that this error occurred due to actions of the U.S. Patent and Trademark Office, since the correct sequence listing was provided to the Office and considered by the examiner during prosecution. Accordingly, patentees request that the sequence listing be corrected as follows:

Column 73, line 21, delete the entire sequence listing through column 84, line 19 and insert

--SEQUENCE LISTING

<210> 1
<211> 5
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(5)
<223> Heavy Chain complementarity determinng region 1 (CDR1).

<400> 1

Ser Tyr Ala Met His
1 5

<210> 2
<211> 17
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)..(17)
<223> Heavy Chain complementarity determinng region 2 (CDR2).

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> Xaa at position 1 is selected from Ile, Phe or Val.

<220>

<221> MISC_FEATURE

<222> (2)..(2)

<223> Xaa at position 2 is selected from Ile or Met.

<220>

<221> MISC_FEATURE

<222> (3)..(3)

<223> Xaa at position 3 is selected from Ser or Leu.

<220>

<221> MISC_FEATURE

<222> (4)..(4)

<223> Xaa at position 4 is selected from Tyr or Phe.

<220>

<221> MISC_FEATURE

<222> (10)..(10)

<223> Xaa at position 10 is selected from Lys or Tyr.

<220>

<221> MISC_FEATURE

<222> (11)..(11)

<223> Xaa at position 11 is selected from Ser or Tyr.

<220>

<221> MISC_FEATURE

<222> (17)..(17)

<223> Xaa at position 17 is selected from Asp or Gly.

<400> 2

Xaa Xaa Xaa Xaa Asp Gly Ser Asn Lys Xaa Xaa Ala Asp Ser Val Lys Xaa
1 5 10 15

<210> 3
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(17)
<223> Heavy Chain complementarity determinng region 3 (CDR3).

<220>
<221> MISC_FEATURE
<222> (4)..(4)
<223> Xaa at position 4 is selected from Ile or Val.

<220>
<221> MISC_FEATURE
<222> (5)..(5)
<223> Xaa at position 5 is selected from Ser, Ala or Gly.

<220>
<221> MISC_FEATURE
<222> (9)..(9)
<223> Xaa at position 9 is selected from Asn or Tyr.

<400> 3

Asp Arg Gly Xaa Xaa Ala Gly Gly Xaa Tyr Tyr Tyr Tyr Gly Met Asp Val
1 5 10 15

<210> 4
<211> 11
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(11)
<223> Light Chain complementarity determinng region 1 (CDR1).

<220>
<221> MISC_FEATURE
<222> (7)..(7)
<223> Xaa at position 7 is selected from Ser or Tyr.

<400> 4

Arg Ala Ser Gln Ser Val Xaa Ser Tyr Leu Ala
1 5 10

<210> 5
<211> 7
<212> PRT
<213> Homo sapiens

<220>

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<222> (1)..(7)

<223> Light Chain complementarity determinng region 2 (CDR2).

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Asp Ala Ser Asn Arg Ala Thr
1 5

<210> 6

<211> 10

<212> PRT

<213> Homo sapiens

<220>

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<222> (1)..(10)

<223> Light Chain complementarity determinng region 3 (CDR3).

<400> 6

Gln Gln Arg Ser Asn Trp Pro Pro Phe Thr
1 5 10

<210> 7

<211> 126

<212> PRT

<213> Homo sapiens

<400> 7

Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg

1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr
20 25 30

Ala Met His Trp Val Arg Gln Ala Pro Gly Asn Gly Leu Glu Trp Val
35 40 45

Ala Phe Met Ser Tyr Asp Gly Ser Asn Lys Lys Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Arg Gly Ile Ala Ala Gly Gly Asn Tyr Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

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<211> 108
<212> PRT
<213> Homo sapiens
<400> 8

Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly

1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Tyr Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Arg Ser Asn Trp Pro Pro
85 90 95

Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105

<210> 9
<211> 157
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(157)
<223> human TNF alpha monomer sequence

<400> 9

Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val
1 5 10 15

Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg
20 25 30

Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu
35 40 45

Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe
50 55 60

Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
65 70 75 80

Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
85 90 95

Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys
100 105 110

Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys
115 120 125

Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe
130 135 140

Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
145 150 155

<210> 10

<211> 18

<212> DNA

<213> Homo sapiens

<400> 10

ttggtccagt cggactgg 18

<210> 11

<211> 18

<212> DNA

<213> Homo sapiens

<400> 11

cacctgcact cggtgctt 18

<210> 12

<211> 30

<212> DNA

<213> Homo sapiens

<400> 12

cactgttttg agtgtgtacg ggcttaagtt 30

<210> 13

<211> 18

<212> DNA

<213> Homo sapiens

<400> 13

gccgcacgtg tggaaggg 18

<210> 14
<211> 25
<212> DNA
<213> Homo sapiens

<400> 14

agtcaaggtc ggactggctt aagtt 25

<210> 15
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<212> DNA
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<400> 15

gttgtcccct ctcacaatct tcgaattt 28

<210> 16
<211> 18
<212> DNA
<213> Homo sapiens

<400> 16

ggcggtagac tactcgtc 18

<210> 17

<211> 7

<212> PRT

<213> Homo sapiens

<400> 17

Met Asp Trp Thr Trp Ser Ile
1 5

<210> 18

<211> 35

<212> DNA

<213> Homo sapiens

<400> 18

tttcgtacgc caccatggac tggacctgga gcatc 35

<210> 19

<211> 34

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tttcgtacgc caccatgggg tttgggctga gctg 34

<210> 20

<211> 35

<212> DNA

<213> Homo sapiens

<400> 20

tttcgtacgc caccatggag tttgggctga gcatg 35

<210> 21
<211> 35
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<400> 21

tttcgtacgc caccatgaaa cacctgtggt tcttc 35

<210> 22
<211> 35
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<400> 22

tttcgtacgc caccatgggg tcaaccgcca tcctc 35

<210> 23
<211> 6
<212> PRT
<213> Homo sapiens

<400> 23

Thr Val Thr Val Ser Ser
1 5

<210> 24

<211> 36

<212> DNA

<213> Homo sapiens

<400> 24

gtgccagtgg cagaggagtc cattcaagct taagtt 36

<210> 25

<211> 5

<212> PRT

<213> Homo sapiens

<400> 25

Met Asp Met Arg Val
1 5

<210> 26

<211> 31

<212> DNA

<213> Homo sapiens

<400> 26

tttgtcgaca ccatggacat gagggtcctc c 31

<210> 27

<211> 28

<212> DNA

<213> Homo sapiens

<400> 27

tttgtcgaca ccatggaagc cccagctc 28

<210> 28
<211> 6
<212> PRT
<213> Homo sapiens

<400> 28

Thr Lys Val Asp Ile Lys
1 5

<210> 29
<211> 41
<212> DNA
<213> Homo sapiens

<400> 29

ctggtttcac ctatagtttg cattcagaat tcggcgcctt t 41

<210> 30
<211> 35
<212> DNA
<213> Homo sapiens

<400> 30

catctccaga gacaattcca agaacacgct gtatc 35

<210> 31
<211> 35
<212> DNA
<213> Homo sapiens

<400> 31

gtagaggtct ctgttaaggt tcttgtgcga catag 35

<210> 32
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(19)
<223> Signal sequence for heavy chain variable region sequences as presented in original Figure 4

<400> 32

Met Gly Phe Gly Leu Ser Trp Val Phe Leu Val Ala Leu Leu Arg Gly
1 5 10 15

Val Gln Cys

<210> 33

<211> 20

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(20)

<223> Signal sequence for light chain variable region sequences as presented in original Figure 5

<400> 33

Met Glu Ala Pro Ala Gln Leu Leu Phe Leu Leu Leu Leu Trp Leu Pro
1 5 10 15

Asp Thr Thr Gly
20

<210> 34

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(421)

<223> heavy chain variable region DNA sequences as presented in original Figure 2A-2B

<400> 34

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tgtgcagcct ctggttcacc ttcagtagct atgctatgca ctgggtccgc caggctccgg 180
caaggggctg gagtgggtgg cagttatatc atatgatgga aaataaatac tacgcagact 240
ccgtgaaggg ccgattcacc atctagagac aattccaaga acacgctgta tctgcaaatg 300
aacagccaga gctgaggaca cggctgtgta ttactgtgcg agagatcgag gtatatcagc 360
aggtggaata ctactactac tacggtatgg acgtctgggg gcaagggacc acggtcaccg 420
tctcctca 428

<210> 35
<211> 387
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(387)
<223> light chain variable region DNA sequences as presented in original Figure 3

<400> 35

atggaagccc cagctcagct tctcttcctc ctgctactct ggctcccaga taccaccgga 60
gaaattgtgt tgacacagtc tccagccacc ctgtctttgt ctccagggga aagagccacc 120
ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca acagaaacct 180
ggccaggctc ccaggctcct catctatgat gcatccaaca gggccactgg catcccagcc 240
aggttcagtg gcagtgggtc tgggacagac ttcactctca ccatcagcag cctagagcct 300
gaagattttg cagtttatta ctgtcagcag cgtagcaact ggcctccatt cactttcggc 360
cctgggacca aagtggatat caaacgt 387 --

Since the errors needing correction were due to U.S. Patent and Trademark Office mistakes, no fee is due under 35 U.S.C. §254. Should any fees be due for entry and consideration of this Certificate of Correction that have not bee accounted for, the

Commissioner is hereby authorized to charge Johnson & Johnson Deposit Account No. 10-0750/CEN0250NP/KJD. If there are any additional charges or credits in connection with this filing, the Commissioner is hereby authorized to charge/credit the Johnson & Johnson deposit account listed above.

Respectfully submitted,

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Reg. No. 32,890

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Dated: March 25, 2009